

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/510,716

Source: PC7/10

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PCT

## RAW SEQUENCE LISTING

DATE: 07/12/2005

PATENT APPLICATION: US/10/510,716

TIME: 09:41:47

Input Set : A:\260068US0PCT.ST25.txt

Output Set: N:\CRF4\07122005\J510716.raw

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3 <110> APPLICANT: HAKAMADA, YOSHIHIRO
4      OZAWA, TADAHIRO
5      KOBAYASHI, TOORU
7 <120> TITLE OF INVENTION: MUTATED ALKALINE CELLULASE
9 <130> FILE REFERENCE: 260068US0PCT
11 <140> CURRENT APPLICATION NUMBER: 10/510,716
12 <141> CURRENT FILING DATE: 2004-10-18
14 <150> PRIOR APPLICATION NUMBER: PCT/JP03/05371
15 <151> PRIOR FILING DATE: 2003-04-25
17 <150> PRIOR APPLICATION NUMBER: JP 2002-124474
18 <151> PRIOR FILING DATE: 2002-04-25
20 <160> NUMBER OF SEQ ID NOS: 9
22 <170> SOFTWARE: PatentIn version 3.3
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 2475
26 <212> TYPE: DNA
27 <213> ORGANISM: Bacillus sp. KSM-S237
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31 <221> NAME/KEY: CDS
32 <222> LOCATION: (1)..(2475)
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37 1          5          10          15
39 tta gtt tta ctt cta tct tta ttt ccg gca gct ctt gca gca gaa gga      96
40 Leu Val Leu Leu Ser Leu Phe Pro Ala Ala Leu Ala Ala Glu Gly
41          20          25          30
43 aac act cgt gaa gac aat ttt aaa cat tta tta ggt aat gac aat gtt      144
44 Asn Thr Arg Glu Asp Asn Phe Lys His Leu Leu Gly Asn Asp Asn Val
45          35          40          45
47 aaa cgc cct tct gag gct ggc gca tta caa tta caa gaa gtc gat gga      192
48 Lys Arg Pro Ser Glu Ala Gly Ala Leu Gln Leu Gln Glu Val Asp Gly
49          50          55          60
51 caa atg aca tta gta gat caa cat gga gaa aaa att caa tta cgt gga      240
52 Gln Met Thr Leu Val Asp Gln His Gly Glu Lys Ile Gln Leu Arg Gly
53 65          70          75          80
55 atg agt aca cac gga tta cag tgg ttt cct gag atc ttg aat gat aac      288
56 Met Ser Thr His Gly Leu Gln Trp Phe Pro Glu Ile Leu Asn Asp Asn
57          85          90          95
59 gca tac aaa gct ctt tct aac gat tgg gat tcc aat atg att cgt ctt      336
60 Ala Tyr Lys Ala Leu Ser Asn Asp Trp Asp Ser Asn Met Ile Arg Leu
61          100          105          110
63 gct atg tat gta ggt gaa aat ggg tac gct aca aac cct gag tta atc      384

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64 Ala Met Tyr Val Gly Glu Asn Gly Tyr Ala Thr Asn Pro Glu Leu Ile
65      115      120      125
67 aaa caa aga gtg att gat gga att gag tta gcg att gaa aat gac atg      432
68 Lys Gln Arg Val Ile Asp Gly Ile Glu Leu Ala Ile Glu Asn Asp Met
69      130      135      140
71 tat gtt att gtt gac tgg cat gtt cat gcg cca ggt gat cct aga gat      480
72 Tyr Val Ile Val Asp Trp His Val His Ala Pro Gly Asp Pro Arg Asp
73 145      150      155      160
75 cct gtt tat gca ggt gct aaa gat ttc ttt aga gaa att gca gct tta      528
76 Pro Val Tyr Ala Gly Ala Lys Asp Phe Phe Arg Glu Ile Ala Ala Leu
77      165      170      175
79 tac cct aat aat cca cac att att tat gag tta gcg aat gag ccg agt      576
80 Tyr Pro Asn Asn Pro His Ile Ile Tyr Glu Leu Ala Asn Glu Pro Ser
81      180      185      190
83 agt aat aat aat ggt gga gca ggg att ccg aat aac gaa gaa ggt tgg      624
84 Ser Asn Asn Asn Gly Gly Ala Gly Ile Pro Asn Asn Glu Glu Gly Trp
85      195      200      205
87 aaa gcg gta aaa gaa tat gct gat cca att gta gaa atg tta cgt aaa      672
88 Lys Ala Val Lys Glu Tyr Ala Asp Pro Ile Val Glu Met Leu Arg Lys
89      210      215      220
91 agc ggt aat gca gat gac aac att atc att gtt ggt agt cca aac tgg      720
92 Ser Gly Asn Ala Asp Asp Asn Ile Ile Ile Val Gly Ser Pro Asn Trp
93 225      230      235      240
95 agt cag cgt ccg gac tta gca gct gat aat cca att gat gat cac cat      768
96 Ser Gln Arg Pro Asp Leu Ala Ala Asp Asn Pro Ile Asp Asp His His
97      245      250      255
99 aca atg tat act gtt cac ttc tac act ggt tca cat gct gct tca act      816
100 Thr Met Tyr Thr Val His Phe Tyr Thr Gly Ser His Ala Ala Ser Thr
101      260      265      270
103 gaa agc tat ccg tct gaa act cct aac tct gaa aga gga aac gta atg      864
104 Glu Ser Tyr Pro Ser Glu Thr Pro Asn Ser Glu Arg Gly Asn Val Met
105      275      280      285
107 agt aac act cgt tat gcg tta gaa aac gga gta gcg gta ttt gca aca      912
108 Ser Asn Thr Arg Tyr Ala Leu Glu Asn Gly Val Ala Val Phe Ala Thr
109      290      295      300
111 gag tgg gga acg agt caa gct agt gga gac ggt ggt cct tac ttt gat      960
112 Glu Trp Gly Thr Ser Gln Ala Ser Gly Asp Gly Gly Pro Tyr Phe Asp
113 305      310      315      320
115 gaa gca gat gta tgg att gaa ttt tta aat gaa aac aac att agc tgg      1008
116 Glu Ala Asp Val Trp Ile Glu Phe Leu Asn Glu Asn Asn Ile Ser Trp
117      325      330      335
119 gct aac tgg tct tta acg aat aaa aat gaa gta tct ggt gca ttt aca      1056
120 Ala Asn Trp Ser Leu Thr Asn Lys Asn Glu Val Ser Gly Ala Phe Thr
121      340      345      350
123 cca ttc gag tta ggt aag tct aac gca acc aat ctt gac cca ggt cca      1104
124 Pro Phe Glu Leu Gly Lys Ser Asn Ala Thr Asn Leu Asp Pro Gly Pro
125      355      360      365
127 gat cat gtg tgg gca cca gaa gaa tta agt ctt tct gga gaa tat gta      1152
128 Asp His Val Trp Ala Pro Glu Glu Leu Ser Leu Ser Gly Glu Tyr Val

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129	370	375	380	
131	cgt gct cgt att aaa ggt gtg aac tat gag cca atc gac cgt aca aaa	1200		
132	Arg Ala Arg Ile Lys Gly Val Asn Tyr Glu Pro Ile Asp Arg Thr Lys			
133	385 390 395 400			
135	tac acg aaa gta ctt tgg gac ttt aat gat gga acg aag caa gga ttt	1248		
136	Tyr Thr Lys Val Leu Trp Asp Phe Asn Asp Gly Thr Lys Gln Gly Phe			
137	405 410 415			
139	gga gtg aat tcg gat tct cca aat aaa gaa ctt att gca gtt gat aat	1296		
140	Gly Val Asn Ser Asp Ser Pro Asn Lys Glu Leu Ile Ala Val Asp Asn			
141	420 425 430			
143	gaa aac aac act ttg aaa gtt tcg gga tta gat gta agt aac gat gtt	1344		
144	Glu Asn Asn Thr Leu Lys Val Ser Gly Leu Asp Val Ser Asn Asp Val			
145	435 440 445			
147	tca gat ggc aac ttc tgg gct aat gct cgt ctt tct gcc aac ggt tgg	1392		
148	Ser Asp Gly Asn Phe Trp Ala Asn Ala Arg Leu Ser Ala Asn Gly Trp			
149	450 455 460			
151	gga aaa agt gtt gat att tta ggt gct gag aag ctt aca atg gat gtt	1440		
152	Gly Lys Ser Val Asp Ile Leu Gly Ala Glu Lys Leu Thr Met Asp Val			
153	465 470 475 480			
155	att gtt gat gaa cca acg acg gta gct att gcg gcg att cca caa agt	1488		
156	Ile Val Asp Glu Pro Thr Thr Val Ala Ile Ala Ala Ile Pro Gln Ser			
157	485 490 495			
159	agt aaa agt gga tgg gca aat cca gag cgt gct gtt cga gtg aac gcg	1536		
160	Ser Lys Ser Gly Trp Ala Asn Pro Glu Arg Ala Val Arg Val Asn Ala			
161	500 505 510			
163	gaa gat ttt gtc cag caa acg gac ggt aag tat aaa gct gga tta aca	1584		
164	Glu Asp Phe Val Gln Gln Thr Asp Gly Lys Tyr Lys Ala Gly Leu Thr			
165	515 520 525			
167	att aca gga gaa gat gct cct aac cta aaa aat atc gct ttt cat gaa	1632		
168	Ile Thr Gly Glu Asp Ala Pro Asn Leu Lys Asn Ile Ala Phe His Glu			
169	530 535 540			
171	gaa gat aac aat atg aac aac atc att ctg ttc gtg gga act gat gca	1680		
172	Glu Asp Asn Asn Met Asn Asn Ile Ile Leu Phe Val Gly Thr Asp Ala			
173	545 550 555 560			
175	gct gac gtt att tac tta gat aac att aaa gta att gga aca gaa gtt	1728		
176	Ala Asp Val Ile Tyr Leu Asp Asn Ile Lys Val Ile Gly Thr Glu Val			
177	565 570 575			
179	gaa att cca gtt gtt cat gat cca aaa gga gaa gct gtt ctt cct tct	1776		
180	Glu Ile Pro Val Val His Asp Pro Lys Gly Glu Ala Val Leu Pro Ser			
181	580 585 590			
183	gtt ttt gaa gac ggt aca cgt caa ggt tgg gac tgg gct gga gag tct	1824		
184	Val Phe Glu Asp Gly Thr Arg Gln Gly Trp Asp Trp Ala Gly Glu Ser			
185	595 600 605			
187	ggt gtg aaa aca gct tta aca att gaa gaa gca aac ggt tct aac gcg	1872		
188	Gly Val Lys Thr Ala Leu Thr Ile Glu Glu Ala Asn Gly Ser Asn Ala			
189	610 615 620			
191	tta tca tgg gaa ttt gga tat cca gaa gta aaa cct agt gat aac tgg	1920		
192	Leu Ser Trp Glu Phe Gly Tyr Pro Glu Val Lys Pro Ser Asp Asn Trp			
193	625 630 635 640			

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196 Ala Thr Ala Pro Arg Leu Asp Phe Trp Lys Ser Asp Leu Val Arg Gly
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199 gag aat gat tat gta gct ttt gat ttc tat cta gat cca gtt cgt gca      2016
200 Glu Asn Asp Tyr Val Ala Phe Asp Phe Tyr Leu Asp Pro Val Arg Ala
201          660          665          670
203 aca gaa ggc gca atg aat atc aat tta gta ttc cag cca cct act aac      2064
204 Thr Glu Gly Ala Met Asn Ile Asn Leu Val Phe Gln Pro Pro Thr Asn
205          675          680          685
207 ggg tat tgg gta caa gca cca aaa acg tat acg att aac ttt gat gaa      2112
208 Gly Tyr Trp Val Gln Ala Pro Lys Thr Tyr Thr Ile Asn Phe Asp Glu
209          690          695          700
211 tta gag gaa gcg aat caa gta aat ggt tta tat cac tat gaa gtg aaa      2160
212 Leu Glu Glu Ala Asn Gln Val Asn Gly Leu Tyr His Tyr Glu Val Lys
213 705          710          715          720
215 att aac gta aga gat att aca aac att caa gat gac acg tta cta cgt      2208
216 Ile Asn Val Arg Asp Ile Thr Asn Ile Gln Asp Asp Thr Leu Leu Arg
217          725          730          735
219 aac atg atg atc att ttt gca gat gta gaa agt gac ttt gca ggg aga      2256
220 Asn Met Met Ile Ile Phe Ala Asp Val Glu Ser Asp Phe Ala Gly Arg
221          740          745          750
223 gtc ttt gta gat aat gtt cgt ttt gag ggg gct gct act act gag ccg      2304
224 Val Phe Val Asp Asn Val Arg Phe Glu Gly Ala Ala Thr Thr Glu Pro
225          755          760          765
227 gtt gaa cca gag cca gtt gat cct ggc gaa gag acg cca cct gtc gat      2352
228 Val Glu Pro Glu Pro Val Asp Pro Gly Glu Glu Thr Pro Pro Val Asp
229          770          775          780
231 gag aag gaa gcg aaa aaa gaa caa aaa gaa gca gag aaa gaa gag aaa      2400
232 Glu Lys Glu Ala Lys Lys Glu Gln Lys Glu Ala Glu Lys Glu Glu Lys
233 785          790          795          800
235 gaa gca gta aaa gaa gaa aag aaa gaa gct aaa gaa gaa aag aaa gca      2448
236 Glu Ala Val Lys Glu Lys Lys Glu Ala Lys Glu Glu Lys Lys Ala
237          805          810          815
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240 Val Lys Asn Glu Ala Lys Lys Lys
241          820
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245 <211> LENGTH: 824
246 <212> TYPE: PRT
247 <213> ORGANISM: Bacillus sp. KSM-S237
249 <400> SEQUENCE: 2
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256          20          25          30
259 Asn Thr Arg Glu Asp Asn Phe Lys His Leu Leu Gly Asn Asp Asn Val
260          35          40          45
263 Lys Arg Pro Ser Glu Ala Gly Ala Leu Gln Leu Gln Glu Val Asp Gly
264          50          55          60

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267 Gln Met Thr Leu Val Asp Gln His Gly Glu Lys Ile Gln Leu Arg Gly
268 65          70          75          80
271 Met Ser Thr His Gly Leu Gln Trp Phe Pro Glu Ile Leu Asn Asp Asn
272          85          90          95
275 Ala Tyr Lys Ala Leu Ser Asn Asp Trp Asp Ser Asn Met Ile Arg Leu
276          100         105         110
279 Ala Met Tyr Val Gly Glu Asn Gly Tyr Ala Thr Asn Pro Glu Leu Ile
280          115         120         125
283 Lys Gln Arg Val Ile Asp Gly Ile Glu Leu Ala Ile Glu Asn Asp Met
284          130         135         140
287 Tyr Val Ile Val Asp Trp His Val His Ala Pro Gly Asp Pro Arg Asp
288 145          150         155         160
291 Pro Val Tyr Ala Gly Ala Lys Asp Phe Phe Arg Glu Ile Ala Ala Leu
292          165         170         175
295 Tyr Pro Asn Asn Pro His Ile Ile Tyr Glu Leu Ala Asn Glu Pro Ser
296          180         185         190
299 Ser Asn Asn Asn Gly Gly Ala Gly Ile Pro Asn Asn Glu Glu Gly Trp
300          195         200         205
303 Lys Ala Val Lys Glu Tyr Ala Asp Pro Ile Val Glu Met Leu Arg Lys
304          210         215         220
307 Ser Gly Asn Ala Asp Asp Asn Ile Ile Ile Val Gly Ser Pro Asn Trp
308 225          230         235         240
311 Ser Gln Arg Pro Asp Leu Ala Ala Asp Asn Pro Ile Asp Asp His His
312          245         250         255
315 Thr Met Tyr Thr Val His Phe Tyr Thr Gly Ser His Ala Ala Ser Thr
316          260         265         270
319 Glu Ser Tyr Pro Ser Glu Thr Pro Asn Ser Glu Arg Gly Asn Val Met
320          275         280         285
323 Ser Asn Thr Arg Tyr Ala Leu Glu Asn Gly Val Ala Val Phe Ala Thr
324          290         295         300
327 Glu Trp Gly Thr Ser Gln Ala Ser Gly Asp Gly Gly Pro Tyr Phe Asp
328 305          310         315         320
331 Glu Ala Asp Val Trp Ile Glu Phe Leu Asn Glu Asn Asn Ile Ser Trp
332          325         330         335
335 Ala Asn Trp Ser Leu Thr Asn Lys Asn Glu Val Ser Gly Ala Phe Thr
336          340         345         350
339 Pro Phe Glu Leu Gly Lys Ser Asn Ala Thr Asn Leu Asp Pro Gly Pro
340          355         360         365
343 Asp His Val Trp Ala Pro Glu Glu Leu Ser Leu Ser Gly Glu Tyr Val
344          370         375         380
347 Arg Ala Arg Ile Lys Gly Val Asn Tyr Glu Pro Ile Asp Arg Thr Lys
348 385          390         395         400
351 Tyr Thr Lys Val Leu Trp Asp Phe Asn Asp Gly Thr Lys Gln Gly Phe
352          405         410         415
355 Gly Val Asn Ser Asp Ser Pro Asn Lys Glu Leu Ile Ala Val Asp Asn
356          420         425         430
359 Glu Asn Asn Thr Leu Lys Val Ser Gly Leu Asp Val Ser Asn Asp Val
360          435         440         445
363 Ser Asp Gly Asn Phe Trp Ala Asn Ala Arg Leu Ser Ala Asn Gly Trp

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**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/510,716

DATE: 07/12/2005

TIME: 09:41:48

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